

1600

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/835,381

DATE: 08/22/2001  
TIME: 10:33:35

Input Set : A:\ES.txt  
Output Set: N:\CRF3\08222001\I835381.raw

3 <110> APPLICANT: SUGA, Mikiko  
4 ASAKURA, Yoko  
5 MORI, Yukiko  
6 ITO, Hisao  
7 KURAHASHI, Osamu  
9 <120> TITLE OF INVENTION: ARGININE REPRESSOR DEFICIENT STRAIN OF CORYNEFORM BACTERIUM  
AND METHOD

ENTERED

10 FOR PRODUCING L-ARGININE  
12 <130> FILE REFERENCE: 206018US0  
14 <140> CURRENT APPLICATION NUMBER: 09/835,381  
15 <141> CURRENT FILING DATE: 2001-04-17  
17 <150> PRIOR APPLICATION NUMBER: JP2000-129167  
18 <151> PRIOR FILING DATE: 2000-04-28  
20 <160> NUMBER OF SEQ ID NOS: 22  
22 <170> SOFTWARE: PatentIn version 3.1  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 32  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Artificial Sequence  
29 <220> FEATURE:  
30 <223> OTHER INFORMATION: synthetic DNA  
32 <400> SEQUENCE: 1  
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36 <210> SEQ ID NO: 2  
37 <211> LENGTH: 30  
38 <212> TYPE: DNA  
39 <213> ORGANISM: Artificial Sequence  
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44 <400> SEQUENCE: 2  
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48 <210> SEQ ID NO: 3  
49 <211> LENGTH: 26  
50 <212> TYPE: DNA  
51 <213> ORGANISM: Artificial Sequence  
53 <220> FEATURE:  
54 <223> OTHER INFORMATION: synthetic DNA  
56 <400> SEQUENCE: 3  
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60 <210> SEQ ID NO: 4  
61 <211> LENGTH: 25  
62 <212> TYPE: DNA  
63 <213> ORGANISM: Artificial Sequence  
65 <220> FEATURE:  
66 <223> OTHER INFORMATION: synthetic DNA  
68 <400> SEQUENCE: 4  
69 aggccaaaaa ttaaggcagt tattg 25  
72 <210> SEQ ID NO: 5

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73 <211> LENGTH: 4447  
 74 <212> TYPE: DNA  
 75 <213> ORGANISM: Brevibacterium lactofermentum  
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 78 <221> NAME/KEY: CDS  
 79 <222> LOCATION: (1318)..(2598)  
 80 <223> OTHER INFORMATION:  
 83 <400> SEQUENCE: 5  
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 86 tttccctcg tttcccact ttttaatggg ggccgggggt agagctacgc gggccggcgcac 120  
 88 ctgctgcgtc gtgatccaat attcggggtc gttcactggg tccccctttct gatttctggc 180  
 90 atagaagaac ccccgtagaaac ttgtgtggttc cgggggttgc tgatttttgc gagacttctc 240  
 92 ggcataattcc ctagcttagg taaaaaacacc atgaaacact agggaaacac ccatgaaaca 300  
 94 cccattaggg cagtagggcg gttcttcgt ctagggcttg catttggcg gtgatctgg 360  
 96 ctttagcgtg taaaagtgtg tggtaggtgg cgtgctcaat gcactcgaac gtcacgtcat 420  
 98 ttaccgggtc acgggtggca aagagaacta gtgggttaga cattgtttc ctcgttgcg 480  
 100 gtgggtgtga gttttctag ccgtcggtt aacgcggcgta tcatgaactc ttggagggtt 540  
 102 tcaccgttct gcatgcgtc gcgttcatg tcctcacgtt gtgccaagg aacgcgtcg 600  
 104 gtgaccacga cgggcttagc cttgcgtc gcttctagtg ctgcgtatggt ggcttgc 660  
 106 tgcgttgcgtc ggcgttgcgt tgcgttgcgt gcttcttgcgtt gttgctgttgc tagctgtgcc 720  
 108 ttgggtgtcca tgctttaaga ctctagtagc tttctgcgtatgtcatgc gcatgcgttag 780  
 110 caaacattgtt cctgcaactc attcattatg tgcaatgtcgtc ctgttactatg tcgtacatac 840  
 112 tcatatttac ctatgtcgtca tgcgttgcgt gcacatgcgt tcatgtcgtc ctaatgtgt 900  
 114 aaacatgtac atgcagatgg ctgggggtgc agggggcgga gccaccctgtt ccatgcgggg 960  
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 118 cccctaggtt tcggacacgtt aaccctccca tgtcgatgcgtt aatcttttac attggatgtac 1080  
 120 ggttaagctgg cacgcatacg caagcttagc ggccacccaa caccactaaa aattaatagt 1140  
 122 ccctagacaa gacaaacccc cgtgcgttgcgtt accaactcat atgcacgggg gccacataac 1200  
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 126 caaaactcgtca ctgcgttgcgtt ccgcacaaacta tcgggtctgtt gtaacactgtt aatagaa 1317  
 128 gttt aac acc tct aag gaa ccg cag gtc aat gag ggt tct aag gtc act 1365  
 129 Val Asn Thr Ser Lys Glu Pro Gln Val Asn Glu Gly Ser Lys Val Thr  
 130 1 5 10 15  
 132 cgc gct agg gcg tgg cgt agg caa aac gtc atg tac aag atc acc aat 1413  
 133 Arg Ala Arg Ala Trp Arg Arg Gln Asn Val Met Tyr Lys Ile Thr Asn  
 134 20 25 30  
 136 agt aag gct ctg gcg ggg tgc cat agg tgg cgc agg gac gaa gct gtt 1461  
 137 Ser Lys Ala Leu Ala Gly Cys His Arg Trp Arg Arg Asp Glu Ala Val  
 138 35 40 45  
 140 gcg gtg tcc tgg tcg tct aac ggt gct tcg cag ttt gag ggt ctg caa 1509  
 141 Ala Val Ser Trp Ser Ser Asn Gly Ala Ser Gln Phe Glu Gly Leu Gln  
 142 50 55 60  
 144 aac tct cac tct cgc tgg ggg tca cct ctg gct gaa ttg gaa gtc atg 1557  
 145 Asn Ser His Ser Arg Trp Gly Ser Pro Leu Ala Glu Leu Glu Val Met  
 146 65 70 75 80  
 148 ggc gaa cgc cgc att gag ctg gct att gct act aag aat cac ttg gcg 1605  
 149 Gly Glu Arg Arg Ile Glu Leu Ala Ile Ala Thr Lys Asn His Leu Ala  
 150 85 90 95  
 152 gcg ggt ggc gcg ctc atg atg ttt gtg ggc act gtt cga cac aac cgc 1653

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153	Ala	Gly	Gly	Ala	Leu	Met	Met	Phe	Val	Gly	Thr	Val	Arg	His	Asn	Arg		
154				100				105					110					
156	tca	cag	tca	ttt	gcg	cag	gtt	gaa	gcg	ggt	att	aag	act	gcg	tac	tct	1701	
157	Ser	Gln	Ser	Phe	Ala	Gln	Val	Glu	Ala	Gly	Ile	Lys	Thr	Ala	Tyr	Ser		
158		115					120					125						
160	tcg	atg	gtg	aaa	aca	tct	cag	tgg	aag	aaa	gaa	cgt	gca	cg	tac	ggg	1749	
161	Ser	Met	Val	Lys	Thr	Ser	Gln	Trp	Lys	Lys	Glu	Arg	Ala	Arg	Tyr	Gly		
162		130					135				140							
164	gtg	gag	cac	acc	tat	agt	gac	tat	gag	gtc	aca	gac	tct	tgg	gcg	aac	1797	
165	Val	Glu	His	Thr	Tyr	Ser	Asp	Tyr	Glu	Val	Thr	Asp	Ser	Trp	Ala	Asn		
166	145		150						155				160					
168	ggt	tgg	cac	ttg	cac	cgc	aac	atg	ctg	ttg	ttc	ttg	gat	cgt	cca	ctg	1845	
169	Gly	Trp	His	Leu	His	Arg	Asn	Met	Leu	Leu	Phe	Leu	Asp	Arg	Pro	Leu		
170				165				170			175							
172	tct	gac	gat	gaa	ctc	aag	gcg	ttt	gag	gat	tcc	atg	ttt	tcc	cgc	tgg	1893	
173	Ser	Asp	Asp	Glu	Leu	Lys	Ala	Phe	Glu	Asp	Ser	Met	Phe	Ser	Arg	Trp		
174		180					185				190							
176	tct	gct	ggt	gtg	gtt	aag	gcc	ggt	atg	gac	gca	cca	ctg	cgt	gag	cac	1941	
177	Ser	Ala	Gly	Val	Val	Lys	Ala	Gly	Met	Asp	Ala	Pro	Leu	Arg	Glu	His		
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180	ggg	gtc	aaa	ctt	gat	cag	gtg	tct	acc	tgg	ggt	gga	gac	gct	gcg	aaa	1989	
181	Gly	Val	Lys	Leu	Asp	Gln	Val	Ser	Thr	Trp	Gly	Gly	Asp	Ala	Ala	Lys		
182		210					215				220							
184	atg	gca	acc	tac	ctc	gct	aag	ggc	atg	tct	cag	gaa	ctg	act	ggc	tcc	2037	
185	Met	Ala	Thr	Tyr	Leu	Ala	Lys	Gly	Met	Ser	Gln	Glu	Leu	Thr	Gly	Ser		
186	225		230						235				240					
188	gct	act	aaa	acc	gcg	tct	aag	ggg	tcg	tac	acg	ccg	ttt	cag	atg	ttg	2085	
189	Ala	Thr	Lys	Thr	Ala	Ser	Lys	Gly	Ser	Tyr	Thr	Pro	Phe	Gln	Met	Leu		
190							245			250			255					
192	gat	atg	ttg	gcc	gat	caa	agc	gac	gcc	ggc	gag	gat	atg	gac	gct	gtt	2133	
193	Asp	Met	Leu	Ala	Asp	Gln	Ser	Asp	Ala	Gly	Glu	Asp	Met	Asp	Ala	Val		
194		260					265			270								
196	ttg	gtg	gct	cg	ttg	cgt	gag	tat	gag	gtt	ggt	tct	aaa	aac	ctg	cgt	2181	
197	Leu	Val	Ala	Arg	Trp	Arg	Glu	Tyr	Glu	Val	Gly	Ser	Lys	Asn	Leu	Arg		
198		275					280				285							
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204	gac	gct	gat	gta	cgt	cgt	gaa	atg	gaa	gaa	gaa	ctg	tac	aag	ctc	gcc	2277	
205	Asp	Ala	Asp	Val	Arg	Arg	Glu	Met	Glu	Glu	Glu	Leu	Tyr	Lys	Leu	Ala		
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208	ggt	ctg	gaa	gca	ccg	gaa	cg	gtc	gaa	tca	acc	ccg	gtt	gct	gtt	gct	2325	
209	Gly	Leu	Glu	Ala	Pro	Glu	Arg	Val	Glu	Ser	Thr	Arg	Val	Ala	Val	Ala		
210							325			330			335					
212	ttg	gtg	aag	ccc	gat	gat	tgg	aaa	ctg	att	cag	tct	gat	ttc	gcg	gtt	2373	
213	Leu	Val	Lys	Pro	Asp	Asp	Trp	Lys	Leu	Ile	Gln	Ser	Asp	Phe	Ala	Val		
214		340					345				350							
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222	370	375	380	
224	acc ccg tgc atg atc gtt atg gat gat gtg gac ttg gac gcg gtt ctg			2517
225	Thr Pro Cys Met Ile Val Met Asp Asp Val Asp Leu Asp Ala Val Leu			
226	385	390	395	400
228	cct act cat ggg gac gct act aag cgt gat ctg aat gcg gcg gtg ttc			2565
229	Pro Thr His Gly Asp Ala Thr Lys Arg Asp Leu Asn Ala Ala Val Phe			
230	405	410	415	
232	gcg ggt aat gag cag act att ctt cgc acc cac taaaagcggc ataaaccccg			2618
233	Ala Gly Asn Glu Gln Thr Ile Leu Arg Thr His			
234	420	425		
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238	tgttgttgc aatggctgat ttcatcagga atgaaactgt catgcttta tgtgcctggc			2738
240	tcctaatacaa agctggggac aatgggttgc cccgttgc tcatcttagtt cggttggcg			2798
242	gggcttcaact gtatctgggg gtggcatcgta gaatagattt cacaccgtt tggcagtgt			2858
244	gcacaccata gtgggcatga gtaataccata cgcgcgcgtt ggctagggtt taacgcgcgt			2918
246	tttgccgtgc tgcggggcat acgttagcgc atacgccttt ttctgtaaaa ccttttgc			2978
248	tttgttttc gtgttgtttt ctttctgtt ggcggggcaa cttaacgcct gcgggggtgg			3038
250	tttgtgacgt taacgggggtt agttttattt cccctagtttgg tttttcagta cgacaatcg			3098
252	gaaagacctg ttcagccag ttcgggtcat gttcgctggt atggccacgt gcatacgac			3158
254	cagtttgcg gttcaactggg atttttgggtt catcaacaa gatgttagac aatgcgttt			3218
256	ctaggtctac ttttgctttt atgcccgtaca agccccgtgg gtattcagcg attgattcca			3278
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286	ggccctgggtt gttgggttgc ctggggaggt cgtatgtatcc gttgggtgttgc cccgggttgc			4178
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292	cggggagaat gttttttgg gtcatgggtt cttttctgt tgcgttgcgaa gtcgttatgt			4358
294	gggcgttgggaa aagccccggc accctttgg gtcacccggg gctagatagt cgcttgcgatgt			4418
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301	<212> TYPE: PRT			
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306 Val Asn Thr Ser Lys Glu Pro Gln Val Asn Glu Gly Ser Lys Val Thr  
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 311 20 25 30  
 314 Ser Lys Ala Leu Ala Gly Cys His Arg Trp Arg Arg Asp Glu Ala Val  
 315 35 40 45  
 318 Ala Val Ser Trp Ser Ser Asn Gly Ala Ser Gln Phe Glu Gly Leu Gln  
 319 50 55 60  
 322 Asn Ser His Ser Arg Trp Gly Ser Pro Leu Ala Glu Leu Glu Val Met  
 323 65 70 75 80  
 326 Gly Glu Arg Arg Ile Glu Leu Ala Ile Ala Thr Lys Asn His Leu Ala  
 327 85 90 95  
 330 Ala Gly Gly Ala Leu Met Met Phe Val Gly Thr Val Arg His Asn Arg  
 331 100 105 110  
 334 Ser Gln Ser Phe Ala Gln Val Glu Ala Gly Ile Lys Thr Ala Tyr Ser  
 335 115 120 125  
 338 Ser Met Val Lys Thr Ser Gln Trp Lys Lys Glu Arg Ala Arg Tyr Gly  
 339 130 135 140  
 342 Val Glu His Thr Tyr Ser Asp Tyr Glu Val Thr Asp Ser Trp Ala Asn  
 343 145 150 155 160  
 346 Gly Trp His Leu His Arg Asn Met Leu Leu Phe Leu Asp Arg Pro Leu  
 347 165 170 175  
 350 Ser Asp Asp Glu Leu Lys Ala Phe Glu Asp Ser Met Phe Ser Arg Trp  
 351 180 185 190  
 354 Ser Ala Gly Val Val Lys Ala Gly Met Asp Ala Pro Leu Arg Glu His  
 355 195 200 205  
 358 Gly Val Lys Leu Asp Gln Val Ser Thr Trp Gly Gly Asp Ala Ala Lys  
 359 210 215 220  
 362 Met Ala Thr Tyr Leu Ala Lys Gly Met Ser Gln Glu Leu Thr Gly Ser  
 363 225 230 235 240  
 366 Ala Thr Lys Thr Ala Ser Lys Gly Ser Tyr Thr Pro Phe Gln Met Leu  
 367 245 250 255  
 370 Asp Met Leu Ala Asp Gln Ser Asp Ala Gly Glu Asp Met Asp Ala Val  
 371 260 265 270  
 374 Leu Val Ala Arg Trp Arg Glu Tyr Glu Val Gly Ser Lys Asn Leu Arg  
 375 275 280 285  
 378 Ser Ser Trp Ser Arg Gly Ala Lys Arg Ala Leu Gly Ile Asp Tyr Ile  
 379 290 295 300  
 382 Asp Ala Asp Val Arg Arg Glu Met Glu Glu Leu Tyr Lys Leu Ala  
 383 305 310 315 320  
 386 Gly Leu Glu Ala Pro Glu Arg Val Glu Ser Thr Arg Val Ala Val Ala  
 387 325 330 335  
 390 Leu Val Lys Pro Asp Asp Trp Lys Leu Ile Gln Ser Asp Phe Ala Val  
 391 340 345 350  
 394 Arg Gln Tyr Val Leu Asp Cys Val Asp Lys Ala Lys Asp Val Ala Ala  
 395 355 360 365  
 398 Ala Gln Arg Val Ala Asn Glu Val Leu Ala Ser Leu Gly Val Asp Ser  
 399 370 375 380  
 402 Thr Pro Cys Met Ile Val Met Asp Asp Val Asp Leu Asp Ala Val Leu

**VERIFICATION SUMMARY**

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